#12
4/7/99

see p.5

ENTERED

1	<110> APPLICANT: Shyjan, Andrew W.
2	<120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
3	AND TREATMENT OF TUMOR PROGRESSION
4	<130> FILE REFERENCE: 07334/004002
5	<140> CURRENT APPLICATION NUMBER: US/08/862,442A
6	<141> CURRENT FILING DATE: 1997-05-23
7	<150> EARLIER APPLICATION NUMBER: US 08/623,679
8	<151> EARLIER FILING DATE: 1996-03-29
9	<160> NUMBER OF SEQ ID NOS: 9
10	<170> SOFTWARE: FastSEQ for Windows Version 3.0
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13	<212> TYPE: DNA
14	<213> ORGANISM: Mus musculus
15	<400> SEQUENCE: 1

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18      ctgtgcctcc cagagtaaca tgtggttcct tgatgtgctt ccccaaaagc ccacctgtgc     180
19      agaatg                                                               186
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25	<221> NAME/KEY: CDS
26	<222> LOCATION: (321)...(1946)
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30      ctaacagatg ttgctgtggt cagctcacta accagcacat cccccctttg ccgagtgggg     180
31      ctcccagcac aacaggagag gacaccaagc aggcagacac gcagtccggg aaatggtctg     240
32      tcagcaaaca cacccagagc tacccaacag actcctatgg gattcttgaa ttccagggtg     300
33      ggggttactc caataaagcc atg tac atc cga gtc tcc tac gac acc aag cca     353
34                                 Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys Pro
35                                  1               5                   10

36      gat tcc ctg ctc cac ctc atg gtg aag gac tgg cag ctg gag ctc ccg     401
37      Asp Ser Leu Leu His Leu Met Val Lys Asp Trp Gln Leu Glu Leu Pro
38                  15                  20                  25

39      aag ctc ttg ata tct gtg cac gga ggc ctc caa agc ttc gag atg cag     449
40      Lys Leu Leu Ile Ser Val His Gly Gly Leu Gln Ser Phe Glu Met Gln
41                  30                  35                  40

42      tcc aaa ctg aag cag gtg ttt ggg aaa ggt ctg atc aag gct gcc atg     497
43      Ser Lys Leu Lys Gln Val Phe Gly Lys Gly Leu Ile Lys Ala Ala Met
44                  45                  50                  55
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45      acc acg ggg gcg tgg atc ttc acc ggg ggt gtg agc act ggt gtc gtc    545
46      Thr Thr Gly Ala Trp Ile Phe Thr Gly Gly Val Ser Thr Gly Val Val
47           60              65              70              75
48      agc cat gtg ggg gat gcc ttg aaa gac cac tcc tcc aag tcc aga ggc    593
49      Ser His Val Gly Asp Ala Leu Lys Asp His Ser Ser Lys Ser Arg Gly
50               80              85              90
51      cgg ctc tgt gct ata gga att gct ccc tgg ggc atg gtg gag aac aag    641
52      Arg Leu Cys Ala Ile Gly Ile Ala Pro Trp Gly Met Val Glu Asn Lys
53               95             100             105
54      gaa gac ctg att gga aaa gat gta aca aga gtc tat cag acc atg tcc    689
55      Glu Asp Leu Ile Gly Lys Asp Val Thr Arg Val Tyr Gln Thr Met Ser
56               110             115             120
57      aac cct ctg agc aag ctc tct gtg ctc aac aat tcc cac act cac ttc    737
58      Asn Pro Leu Ser Lys Leu Ser Val Leu Asn Asn Ser His Thr His Phe
59           125             130             135
60      atc ttg gct gac aac ggc acc ctg ggc aag tat ggt gct gag gtg aag    785
61      Ile Leu Ala Asp Asn Gly Thr Leu Gly Lys Tyr Gly Ala Glu Val Lys
62      140             145             150             155
63      ctt cga aga cag ctg gaa aaa cac atc tcc ctg cag aag atc aac aca    833
64      Leu Arg Arg Gln Leu Glu Lys His Ile Ser Leu Gln Lys Ile Asn Thr
65               160             165             170
66      agg ctg ggc cag ggt gta cct gtc gtg ggc cta gtg gta gaa ggt ggt    881
67      Arg Leu Gly Gln Gly Val Pro Val Val Gly Leu Val Val Glu Gly Gly
68               175             180             185
69      cct aac gtg gtt tct atc gtc ctg gag tat ctc aaa gaa gac cct cct    929
70      Pro Asn Val Val Ser Ile Val Leu Glu Tyr Leu Lys Glu Asp Pro Pro
71               190             195             200
72      gtc cct gtg gtg gtt tgc gat ggc agt gga cgt gcc tct gac att ttg    977
73      Val Pro Val Val Val Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile Leu
74           205             210             215
75      tcc ttc gca cac aaa tac tgc gac gaa gga gga gtc ata aac gag tcc    1025
76      Ser Phe Ala His Lys Tyr Cys Asp Glu Gly Gly Val Ile Asn Glu Ser
77      220             225             230             235
78      ctg cgg gac cag ctt cta gtt acc att cag aaa aca ttt aat tac agc    1073
79      Leu Arg Asp Gln Leu Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr Ser
80               240             245             250
81      aag tcc cag tcg tat cag ctg ttt gca att atc atg gag tgc atg aag    1121
82      Lys Ser Gln Ser Tyr Gln Leu Phe Ala Ile Ile Met Glu Cys Met Lys
83               255             260             265
84      aag aaa gaa ctc gtc act gtg ttt cgg atg ggt tcc gag ggt cag caa    1169
85      Lys Lys Glu Leu Val Thr Val Phe Arg Met Gly Ser Glu Gly Gln Gln
86               270             275             280
87      gat gtc gag atg gca att tta act gcc ttg ctc aaa gga acc aac gca    1217
88      Asp Val Glu Met Ala Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn Ala
89               285             290             295
90      tca gct cca gat cag ctg agc ttg gcc ctg gct tgg aac cgg gtc gac    1265
91      Ser Ala Pro Asp Gln Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp
92      300             305             310             315
93      ata gcg cga agc cag atc ttc gtc ttt ggc cca cac tgg ccg cca ctg    1313
94      Ile Ala Arg Ser Gln Ile Phe Val Phe Gly Pro His Trp Pro Pro Leu
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 95                          320                325                330
 96         gga agc ctg gcc cct cct gtg gac acc aaa gcc gca gag aag gaa aag    1361
 97         Gly Ser Leu Ala Pro Pro Val Asp Thr Lys Ala Ala Glu Lys Glu Lys
 98                          335                340                345
 99         aag cca ccc aca gcc acc acc aag ggg aga gga aaa gga aaa ggc aag     1409
100         Lys Pro Pro Thr Ala Thr Thr Lys Gly Arg Gly Lys Gly Lys Gly Lys
101                          350                355                360
102         aag aaa ggc aaa gtg aaa gag gaa gtg gag gaa gag acg gac ccc cgg     1457
103         Lys Lys Gly Lys Val Lys Glu Glu Val Glu Glu Glu Thr Asp Pro Arg
104                          365                370                375
105         aag ctt gag ctg ctc aac tgg gtg aat gcc ctg gag caa gcc atg ctg     1505
106         Lys Leu Glu Leu Leu Asn Trp Val Asn Ala Leu Glu Gln Ala Met Leu
107                  380                385                390                395
108         gat gct ctt gtc cta gat cgg gtg gac ttt gta aag ctc ctg att gaa     1553
109         Asp Ala Leu Val Leu Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu
110                          400                405                410
111         aac gga gtg aac atg cag cat ttc ctc acc atc ccg agg ctg gag gag     1601
112         Asn Gly Val Asn Met Gln His Phe Leu Thr Ile Pro Arg Leu Glu Glu
113                          415                420                425
114         cta tac aac acc aga ctg ggc cca cca aac acc ctt cat ctg ctg gtg     1649
115         Leu Tyr Asn Thr Arg Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val
116                  430                435                440
117         cgg gat gta aag aag agc aac ctt cca cct gat tac cac atc agc ctc     1697
118         Arg Asp Val Lys Lys Ser Asn Leu Pro Pro Asp Tyr His Ile Ser Leu
119                  445                450                455
120         att gat ata gga ctg gtg ctg gag tac ctc atg ggc ggt gcc tac cgc     1745
121         Ile Asp Ile Gly Leu Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg
122                  460                465                470                475
123         tgc aac tac act cgg aaa agc ttc cgg act ctc tac aac aac ttg ttt     1793
124         Cys Asn Tyr Thr Arg Lys Ser Phe Arg Thr Leu Tyr Asn Asn Leu Phe
125                          480                485                490
126         ggc cct aag agg gta gag ctc agc aga cac aca gtg tcc tgt gcc tcc     1841
127         Gly Pro Lys Arg Val Glu Leu Ser Arg His Thr Val Ser Cys Ala Ser
128                          495                500                505
129         cag agt aac atg tgg ttc ctt gat gtg ctt ccc caa aag ccc acc tgt     1889
130         Gln Ser Asn Met Trp Phe Leu Asp Val Leu Pro Gln Lys Pro Thr Cys
131                  510                515                520
132         gca gaa tgc aac tct tca cct cac ctg tcc caa act gac atc acc cca     1937
133         Ala Glu Cys Asn Ser Ser Pro His Leu Ser Gln Thr Asp Ile Thr Pro
134                  525                530                535
135         cct ctg ccc tgacacccag tgcagggcct cctagctttc acatgcagcc            1986
136         Pro Leu Pro
137         540
138         attcacatcg cctctcaaga ctgggccagg cagtgcaacc tgtcaagcat gtctgtcctc   2046
139         ccctccttcc tacaatagcc cccctctgg gccccatgcc tctgctctct cagcccgttc    2106
140         tcctccccac tgatcactgg cgctcctgtt gtcttccaag gcaaggaaca aggaaaagca   2166
141         tcttttgcc cacaaaagtt tagggctccc cgctgttcaa ccatagccaa cctcactgta    2226
142         catcggagtc atccaggcca gctgccacac acaagccttc cccaccctat cccaatagac   2286
143         cctattcctc catcaaaatc aaagctaact cctggcctgc acattgcttc ttcttgctc    2346
144         cagcctgtta aacctccaat aaatgtcaga tctgtgggaa gccttcctca ctctcactcc   2406
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145        acagtttgta cagagagcga gagcctcgtt tggttctact tacaaggaag gctttgtgtc   2466
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147        tcacctggat gttgtcatta attaatagtg atacaaaata ttgacacttc ttttcctgct   2586
148        tctttgttat gcagccgaaa gcacttaagc ttctgggaat ggaagtaagt aggacatgtt   2646
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154   <213> ORGANISM: Mus musculus
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159                     20                  25                  30
160        Val His Gly Gly Leu Gln Ser Phe Glu Met Gln Ser Lys Leu Lys Gln
161                 35                  40                  45
162        Val Phe Gly Lys Gly Leu Ile Lys Ala Ala Met Thr Thr Gly Ala Trp
163             50                  55                  60
164        Ile Phe Thr Gly Gly Val Ser Thr Gly Val Val Ser His Val Gly Asp
165         65                  70                  75                  80
166        Ala Leu Lys Asp His Ser Ser Lys Ser Arg Gly Arg Leu Cys Ala Ile
167                     85                  90                  95
168        Gly Ile Ala Pro Trp Gly Met Val Glu Asn Lys Glu Asp Leu Ile Gly
169                 100                 105                 110
170        Lys Asp Val Thr Arg Val Tyr Gln Thr Met Ser Asn Pro Leu Ser Lys
171                 115                 120                 125
172        Leu Ser Val Leu Asn Asn Ser His Thr His Phe Ile Leu Ala Asp Asn
173             130                 135                 140
174        Gly Thr Leu Gly Lys Tyr Gly Ala Glu Val Lys Leu Arg Arg Gln Leu
175         145                 150                 155                 160
176        Glu Lys His Ile Ser Leu Gln Lys Ile Asn Thr Arg Leu Gly Gln Gly
177                     165                 170                 175
178        Val Pro Val Val Gly Leu Val Val Glu Gly Gly Pro Asn Val Val Ser
179                 180                 185                 190
180        Ile Val Leu Glu Tyr Leu Lys Glu Asp Pro Pro Val Pro Val Val Val
181                 195                 200                 205
182        Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile Leu Ser Phe Ala His Lys
183             210                 215                 220
184        Tyr Cys Asp Glu Gly Gly Val Ile Asn Glu Ser Leu Arg Asp Gln Leu
185         225                 230                 235                 240
186        Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr Ser Lys Ser Gln Ser Tyr
187                     245                 250                 255
188        Gln Leu Phe Ala Ile Ile Met Glu Cys Met Lys Lys Lys Glu Leu Val
189                 260                 265                 270
190        Thr Val Phe Arg Met Gly Ser Glu Gly Gln Gln Asp Val Glu Met Ala
191                 275                 280                 285
192        Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn Ala Ser Ala Pro Asp Gln
193             290                 295                 300
194        Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Gln
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1642

PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/862,442A

DATE: 04/07/1999
TIME: 14:45:43

Input Set: H862442A.RAW

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196         Ile Phe Val Phe Gly Pro His Trp Pro Pro Leu Gly Ser Leu Ala Pro
197                             325                      330                      335
198         Pro Val Asp Thr Lys Ala Ala Glu Lys Glu Lys Lys Pro Pro Thr Ala
199                             340                      345                      350
200         Thr Thr Lys Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Gly Lys Val
201                             355                      360                      365
202         Lys Glu Glu Val Glu Glu Glu Thr Asp Pro Arg Lys Leu Glu Leu Leu
203                      370                      375                      380
204         Asn Trp Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val Leu
205         385                      390                      395                      400
206         Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Asn Met
207                             405                      410                      415
208         Gln His Phe Leu Thr Ile Pro Arg Leu Glu Glu Leu Tyr Asn Thr Arg
209                      420                      425                      430
210         Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys Lys
211                      435                      440                      445
212         Ser Asn Leu Pro Pro Asp Tyr His Ile Ser Leu Ile Asp Ile Gly Leu
213                      450                      455                      460
214         Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr Arg
215         465                      470                      475                      480
216         Lys Ser Phe Arg Thr Leu Tyr Asn Asn Leu Phe Gly Pro Lys Arg Val
217                             485                      490                      495
218         Glu Leu Ser Arg His Thr Val Ser Cys Ala Ser Gln Ser Asn Met Trp
219                      500                      505                      510
220         Phe Leu Asp Val Leu Pro Gln Lys Pro Thr Cys Ala Glu Cys Asn Ser
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223                      530                      535                      540
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235  <213> ORGANISM: Artificial Sequence
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741	W	"N" or "Xaa" used: Feature required	actcattata gggntcgagc ggccgcccgg gcaggttt